

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:**

Application Serial Number: 10/564,136  
Source: IEWD  
Date Processed by STIC: 10/31/2006

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. **EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)**
2. **U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314**

Revised 01/10/06

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 10/564,136

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1  Wrapped Nucleics      Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2  Invalid Line Length      The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3  Misaligned Amino Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4  Non-ASCII      The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5  Variable Length      Sequence(s)  contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6  PatentIn 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)  . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7  Skipped Sequences (OLD RULES)      Sequence(s)  missing. If intentional, please insert the following lines for **each** skipped sequence:  
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
 This sequence is intentionally skipped  
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

*27 thru 215*

8  Skipped Sequences (NEW RULES)      Sequence(s)  missing. If intentional, please insert the following lines for **each** skipped sequence.  
 <210> sequence id number  
 <400> sequence id number  
 000

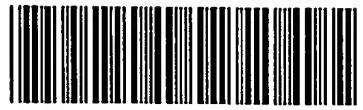
9  Use of n's or Xaa's (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10  Invalid <213> Response      Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

11  Use of <220>      Sequence(s)  missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

12  PatentIn 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13  Misuse of n/Xaa      "n" **can only** represent a single nucleotide; "Xaa" **can only** represent a single amino acid



IFWO

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/564,136

DATE: 10/31/2006  
TIME: 15:10:35

Input Set : A:\10564136.RAW  
Output Set: N:\CRF4\10312006\J564136.raw

3 <110> APPLICANT: Olson-Munoz, Marilyn C.  
4 Curtis, Michelle L.  
5 Ip, Hon S.  
6 Kwiatkowski, Robert W., Jr.  
7 Armantrout, Kyle C.  
8 Cao, Feng  
9 Hurwitz, Bonnie L.  
10 Machmeier, Daniel K.  
11 Olson, Sarah M.  
12 Chehak, LuAnne  
14 <120> TITLE OF INVENTION: Assays for the Direct Measurement of Gene Dosage  
16 <130> FILE REFERENCE: FORS-10718  
C--> 18 <140> CURRENT APPLICATION NUMBER: US/10/564,136  
C--> 18 <141> CURRENT FILING DATE: 2006-01-10  
E--> 18 <160> NUMBER OF SEQ ID NOS: 230 → found 38  
20 <170> SOFTWARE: PatentIn version 3.3

Does Not Comply  
Corrected Diskette Needed

(pg-1)

## ERRORED SEQUENCES

243 <210> SEQ ID NO: 26  
244 <211> LENGTH: 25  
245 <212> TYPE: DNA  
246 <213> ORGANISM: Homo sapiens  
248 <400> SEQUENCE: 26  
E--> 249 cgcgccgagg cctgagcaac gtgca  
E--> 362 <210> SEQ ID NO:  
E--> 362 <211> LENGTH:  
E--> 362 <212> TYPE:  
E--> 362 <213> ORGANISM:  
E--> 362 <400> SEQUENCE: 215 → 27  
363 gagattgtgc acgaggactt gaagatgggg tctgatgggg agagtgcacca ggcttcagcc 60  
365 acgtccctcggtatgagggtgca gtctccagtg a 91  
E--> 368 <210> SEQ ID NO: 216

25 ②

Missing Sequence from 27 thru 215.

for Intentionally Skipped Sequences.

pls us this format . 210 000 } 400 000 } See Item 8  
on Error  
Summary  
Sheet.

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/31/2006  
PATENT APPLICATION: US/10/564.136 TIME: 15:10:36

Input Set : A:\10564136.RAW  
Output Set: N:\CRF4\10312006\J564136.raw

### Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:26; Line(s) 249,250,251,252,253,254,255,256,257,258,259,260,261,262  
Seq#:26; Line(s) 263,264,265,266,267,268,269,270,271,272,273,274,275,276  
Seq#:26; Line(s) 277,278,279,280,281,282,283,284,285,286,287,288,289,290  
Seq#:26; Line(s) 291,292,293,294,295,296,297,298,299,300,301,302,303,304  
Seq#:26; Line(s) 305,306,307,308,309,310,311,312,313,314,315,316,317,318  
Seq#:26; Line(s) 319,320,321,322,323,324,325,326,327,328,329,330,331,332  
Seq#:26; Line(s) 333,334,335,336,337,338,339,340,341,342,343,344,345,346  
Seq#:26; Line(s) 347,348,349,350,351,352,353,354,355,356,357,358,359,360  
Seq#:26; Line(s) 361

### Skipped Sequences (NEW RULES) :

Sequence(s) missing. If intentional, please use the following format for each skipped sequence.

<210> sequence id number

<400> sequence id number

999

Seq#:27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50  
Seq#:51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74  
Seq#:75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98  
Seq#:99,100,101,102,103,104,105,106,107,108,109,110,111,112,113,114,115,116  
Seq#:117,118,119,120,121,122,123,124,125,126,127,128,129,130,131,132,133,134  
Seq#:135,136,137,138,139,140,141,142,143,144,145,146,147,148,149,150,151,152  
Seq#:153,154,155,156,157,158,159,160,161,162,163,164,165,166,167,168,169,170  
Seq#:171,172,173,174,175,176,177,178,179,180,181,182,183,184,185,186,187,188  
Seq#:189,190,191,192,193,194,195,196,197,198,199,200,201,202,203,204,205,206  
Seq#:207,208,209,210,211,212,213,214,215

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/564,136

DATE: 10/31/2006

TIME: 15:10:36

Input Set : A:\10564136.RAW

Output Set: N:\CRF4\10312006\J564136.raw

L:18 M:270 C: Current Application Number differs, Replaced Current Application No  
L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:187 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (19) SEQUENCE:  
L:249 M:254 E: No. of Bases conflict, LENGTH:Input:2 Counted:25 SEQ:26  
L:362 M:282 E: Numeric Field Identifier Missing, <210> is required.  
L:362 M:282 E: Numeric Field Identifier Missing, <211> is required.  
L:362 M:282 E: Numeric Field Identifier Missing, <212> is required.  
L:362 M:282 E: Numeric Field Identifier Missing, <213> is required.  
L:362 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:26 differs:215  
L:368 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 27 thru 215  
L:18 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (230) Counted (39)